

#4

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/521,478
Source: PJT/10
Date Processed by STIC: 1/28/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

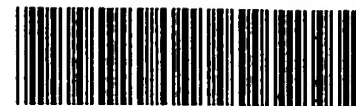
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>101521,498</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>✓</u> <u>Wrapped Nucleics</u> <u>Wrapped Aminos</u>	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>Invalid Line Length</u>	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>Misaligned Amino</u> <u>Numbering</u>	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>Non-ASCII</u>	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>Variable Length</u>	Sequence(s) <u> </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>PatentIn 2.0</u> <u>"bug"</u>	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u> </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>Skipped Sequences</u> <u>(OLD RULES)</u>	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>Skipped Sequences</u> <u>(NEW RULES)</u>	Sequence(s) <u> </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>Use of n's or Xaa's</u> <u>(NEW RULES)</u>	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>Invalid <213></u> <u>Response</u>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>Use of <220></u>	Sequence(s) <u> </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>PatentIn 2.0</u> <u>"bug"</u>	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>Misuse of n/Xaa</u>	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



PCT

RAW SEQUENCE LISTING

DATE: 01/28/2005

PATENT APPLICATION: US/10/521,478

TIME: 11:37:36

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

4 <110> APPLICANT: Michel, Albrecht
 5 Scheffler, Brian E.
 6 Netherland, Michael D.
 7 Dayan, Franck E.
 8 Arias de Ares, Renee S.
 10 <120> TITLE OF INVENTION: HERBICIDE-RESISTANT PLANTS, AND POLYNUCLEOTIDES AND
 11 METHODS FOR PROVIDING SAME
 W--> 13 <130> FILE REFERENCE:
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/521,478
 C--> 16 <141> CURRENT FILING DATE: 2005-01-17
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1982
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Hydrilla verticillata
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (6)..(1748)
 31 <400> SEQUENCE: 1
 E--> 32 caaac atg act gtt gct agg tcg gtc gtt gca gtc aat cta agt ggt tcc
 33 50
 34 Met Thr Val Ala Arg Ser Val Val Ala Val Asn Leu Ser Gly Ser
 35 1 5 10 15
 E--> 37 ctt caa aac aga tac cca gcc agt tca tca gtc agc tgc ttc ctt ggc
 38 98
 39 Leu Gln Asn Arg Tyr Pro Ala Ser Ser Ser Val Ser Cys Phe Leu Gly
 40 20 25 30
 E--> 42 aaa gag tac aga tgc aac agt atg tta gga ttc tgc ggt agt gga aaa
 43 146
 44 Lys Glu Tyr Arg Cys Asn Ser Met Leu Gly Phe Cys Gly Ser Gly Lys
 45 35 40 45
 E--> 47 ttg gct ttt ggc gca aat gca ccc tat tct aag att gca gct acc aaa
 48 194
 49 Leu Ala Phe Gly Ala Asn Ala Pro Tyr Ser Lys Ile Ala Ala Thr Lys
 50 50 55 60
 E--> 52 cca aag ccc aaa ctt cgc cct ttg aag gtc aac tgc atg gat ttc cca
 53 242
 54 Pro Lys Pro Lys Leu Arg Pro Leu Lys Val Asn Cys Met Asp Phe Pro

Does Not Comply
 Corrected Diskette Needed

pp 1-15

(see item 1
 on Error
 Summary Sheet)

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

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55      65      70      75
E--> 59 aga cct gat ata gat aac act gct aat ttc ttg gaa gct gct gct ctt
60 290
61 Arg Pro Asp Ile Asp Asn Thr Ala Asn Phe Leu Glu Ala Ala Ala Leu
62 80      85      90      95
E--> 64 tct tcc tct ttt cgc aat tca gca aga cca agt aaa cct ctt caa gtt
65 338
66 Ser Ser Ser Phe Arg Asn Ser Ala Arg Pro Ser Lys Pro Leu Gln Val
67      100      105      110
E--> 69 gta att gct ggt gca ggt ttg gct ggt ctt tca aca gca aag tat ctc
70 386
71 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
72      115      120      125
E--> 74 gca gat gca ggg cac ata ccc ata cta ctg gag gct aga gat gta ttg
75 434
76 Ala Asp Ala Gly His Ile Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
77      130      135      140
E--> 79 ggt ggc aag gtg gca gcg tgg aaa gat gat gat gga gac tgg tat gag
80 482
81 Gly Gly Lys Val Ala Ala Trp Lys Asp Asp Asp Gly Asp Trp Tyr Glu
82      145      150      155
E--> 84 aca ggc ctg cat ata ttt ttt ggt gca tat ccc aat gtg cag aat tta
85 530
86 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Val Gln Asn Leu
87 160      165      170      175
E--> 89 ttt ggt gaa ctt ggc ata aat gat cgt cta caa tgg aaa gag cat tca
90 578
91 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
92      180      185      190
E--> 94 atg att ttt gcg atg cca aac aag cca ggg gaa ttt agt cgc ttt gat
95 626
96 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp
97      195      200      205
E--> 99 ttt cca gaa gta ctt cct gct cca cta aat gga ata tgg gca atc ctt
100 674
101 Phe Pro Glu Val Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu
102      210      215      220
E--> 104 aaa aac aat gaa atg ctc act tgg cca gag aaa gtg caa ttt gct att
105 722
106 Lys Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Gln Phe Ala Ile
107      225      230      235
E--> 109 gga cta cta cct gca atg att ggg ggg cag cca tat gtt gaa gct cag
110 770
111 Gly Leu Leu Pro Ala Met Ile Gly Gly Gln Pro Tyr Val Glu Ala Gln
112 240      245      250      255
E--> 116 gat ggc tta aca gtt caa gag tgg atg aga aaa cag ggt gtg ccg gat
117 818
118 Asp Gly Leu Thr Val Gln Glu Trp Met Arg Lys Gln Gly Val Pro Asp
119      260      265      270

```

*same
error*

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

E--> 121 cga gtc aat gac gag gtt ttc att gca atg tca aag gct ctt aac ttc
      122 866
      123 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
      124          275          280          285
E--> 126 ata aac cct gat gaa ctt tcc atg caa tgc atc ctg att gcc tta aac
      127 914
      128 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
      129          290          295          300
E--> 131 cgt ttc ctt cag gaa aag cat ggg tgc aag atg gcc ttt tta gat ggt
      132 962
      133 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
      134          305          310          315
E--> 136 aat cca cct gaa aga tta tgt aag cca att gct gat cac atc gag tca
      137 1010
      138 Asn Pro Pro Glu Arg Leu Cys Lys Pro Ile Ala Asp His Ile Glu Ser
      139 320          325          330          335
E--> 141 ttg ggt ggc caa gtc atc ctt aat tcc cga ata cag aag att gag ctg
      142 1058
      143 Leu Gly Gly Gln Val Ile Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
      144          340          345          350
E--> 146 aat gca gac aaa tcc gtc aag cat ttt gtg ctc acc aat gga aat ata
      147 1106
      148 Asn Ala Asp Lys Ser Val Lys His Phe Val Leu Thr Asn Gly Asn Ile
      149          355          360          365
E--> 151 ata aca gga gat gca tat gta ttt gca aca cct gtt gat atc ttg aag
      152 1154
      153 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
      154          370          375          380
E--> 156 ctt ctg tta cct gaa gat tgg aag gag att tca tat ttc aaa aaa ttg
      157 1202
      158 Leu Leu Leu Pro Glu Asp Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu
      159          385          390          395
E--> 161 gac aag ttg gtt ggc gta cct gtg ata aat gta cac ata tgg ttt gat
      162 1250
      163 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
      164 400          405          410          415
E--> 166 agg aag ttg aag aac aca tac gat cat ctt ctt ttc agc agg agt cca
      167 1298
      168 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro
      169          420          425          430
E--> 173 ctg ttg agc gtt tat gca gac atg tct gtt aca tgc aag gaa tac tac
      174 1346
      175 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
      176          435          440          445
E--> 178 aat cca aat caa tcc atg ctt gag cta gta ttt gca cca gca gag aaa
      179 1394
      180 Asn Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Lys
      181          450          455          460
E--> 183 tgg att tca tgc agt gac agt gaa atc att aac gcg act atg caa gag

```

same

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184 1442
185 Trp Ile Ser Cys Ser Asp Ser Glu Ile Ile Asn Ala Thr Met Gln Glu
186      465              470              475
E--> 188 ctt gct aaa ctc ttt cca gat gag att tct gct gat caa agc aag gcc
189 1490
190 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala
191 480              485              490              495
E--> 193 aaa att ttg aaa tat cat gtt gta aag acc ccg agg tca gtt tac aag
194 1538
195 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
196              500              505              510
E--> 198 acg gtc cct gat tgt gaa cca tgc cgg cct ttg caa aga tct cca att
199 1586
200 Thr Val Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile
201              515              520              525
E--> 203 gaa ggg ttc tac ttg gct ggt gac tac aca aag cag aag tat ttg gcc
204 1634
205 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
206              530              535              540
E--> 208 tca atg gaa ggt gcc gtg tta tct ggg aag cta tgt gct cag gca att
209 1682
210 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile
211              545              550              555
E--> 213 gtg cag gac tgc agc ttg ttg gct tct agg gta cag aaa agc cca cag
214 1730
215 Val Gln Asp Cys Ser Leu Leu Ala Ser Arg Val Gln Lys Ser Pro Gln
216 560              565              570              575
E--> 218 acg ttg acg att gcc tga ttcaggaaac ttttatgcag gttcagtttg
219 1778
220 Thr Leu Thr Ile Ala
221              580
E--> 223 tagggggaat atttctgggt ttgtttcatt cagatgtttt tcttttagag catatgtctt
224 1838
E--> 226 tatagtaaaa actccacact ctttctcatg tatagctaca tcagcaagca aagggggtaa
227 1898
E--> 231 gttgcaattt caggacttga acatggcctc tgcacaggta aagacagaat ggacataaat
232 1958
E--> 234 gcaagcatgg aatttacaat attc
235 1982
323 <210> SEQ ID NO: 3
324 <211> LENGTH: 2293
325 <212> TYPE: DNA
326 <213> ORGANISM: Glycine max
328 <220> FEATURE:
329 <221> NAME/KEY: CDS
330 <222> LOCATION: (221)..(1933)
332 <400> SEQUENCE: 3
E--> 333 gaattccttc tacgtactgc cgtgggtgctt tcaccactgc ttaccactaa ccttcctctc
334 60

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*same**same*

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E--> 336 tctctctgcc gctgcaagct tgggtactctc aactcaattc tccaccttat tcttttcaact
      337 120
E--> 339 tcttcagctc ttgttttttc ccaaattctac tttcaaagtg cctgaattct gcaacagtaa
      340 180
E--> 342 tattaacact cctctctttt gttcaggctt tatttcccca atg gcc gct tgt ggc
      343 235
      344
      347 Met Ala Ala Cys Gly
           1 5
E--> 349 tat ata tct gct gcc aac ttc aat tat ctc gtt ggc gcc aga aac ata
      350 283
      351 Tyr Ile Ser Ala Ala Asn Phe Asn Tyr Leu Val Gly Ala Arg Asn Ile
      352 10 15 20
E--> 354 tcc aaa ttc gct tct tca gac gcc aca att tcg ttt tca ttt ggc ggg
      355 331
      356 Ser Lys Phe Ala Ser Ser Asp Ala Thr Ile Ser Phe Ser Phe Gly Gly
      357 25 30 35
E--> 359 agc gac tca atg ggt ctt act ttg cga ccc gct ccg att cgt gct cct
      360 379
      361 Ser Asp Ser Met Gly Leu Thr Leu Arg Pro Ala Pro Ile Arg Ala Pro
      362 40 45 50
E--> 364 aag agg aac cat ttc tct ccc ttg cgt gtc gtt tgc gtc gat tat cca
      365 427
      366 Lys Arg Asn His Phe Ser Pro Leu Arg Val Val Cys Val Asp Tyr Pro
      367 55 60 65
E--> 369 cgc cca gag ctc gaa aac acc gtt aat ttc gtt gaa gct gct tac ttg
      370 475
      371 Arg Pro Glu Leu Glu Asn Thr Val Asn Phe Val Glu Ala Ala Tyr Leu
      372 70 75 80 85
E--> 374 tct tcc acc ttt cgt gct tct ccg cgt cct cta aaa ccc ttg aac atc
      375 523
      376 Ser Ser Thr Phe Arg Ala Ser Pro Arg Pro Leu Lys Pro Leu Asn Ile
      377 90 95 100
E--> 379 gtt att gcc ggt gca gga ttg gct ggt tta tca act gca aaa tat ttg
      380 571
      381 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
      382 105 110 115
E--> 384 gct gat gct ggg cat aaa cct ata ttg ctg gaa gca aga gac gtt cta
      385 619
      386 Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
      387 120 125 130
E--> 389 ggt gga aag gtt gct gca tgg aaa gac aag gat gga gac tgg tac gag
      390 667
      391 Gly Gly Lys Val Ala Ala Trp Lys Asp Lys Asp Gly Asp Trp Tyr Glu
      392 135 140 145
E--> 394 aca ggc cta cac atc ttt ttt ggg gct tac cct tat gtg cag aac ctt
      395 715
      396 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Tyr Val Gln Asn Leu
      397 150 155 160 165
E--> 399 ttt gga gaa ctt ggc att aat gat cgg tta caa tgg aaa gag cat tct

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same

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400 763
401 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
402                170                175                180
E--> 406 atg att ttt gct atg cca aat aag cct gga gag ttt agt cga ttt gat
407 811
408 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp
409                185                190                195
E--> 411 ttt cct gaa gtt ctt ccc tcc cca ttg aat gga ata tgg gca ata ttg
412 859
413 Phe Pro Glu Val Leu Pro Ser Pro Leu Asn Gly Ile Trp Ala Ile Leu
414                200                205                210
E--> 416 agg aac aat gag atg ctt aca tgg cca gag aaa gta aaa ttt gca att
417 907
418 Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Ile
419                215                220                225
E--> 421 ggg ctt ctc cca gct atg ctt ggc gga cag cca tat gtt gag gct caa
422 955
423 Gly Leu Leu Pro Ala Met Leu Gly Gly Gln Pro Tyr Val Glu Ala Gln
424 230                235                240                245
E--> 426 gat ggt ctt tct gtt caa gaa tgg atg aaa aag cag ggc gta cct gaa
427 1003
428 Asp Gly Leu Ser Val Gln Glu Trp Met Lys Lys Gln Gly Val Pro Glu
429                250                255                260
E--> 431 cgg gta gct gat gag gtg ttc ata gca atg tca aag gca cta aac ttc
432 1051
433 Arg Val Ala Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
434                265                270                275
E--> 436 atc aat cct gat gaa ctt tca atg caa tgt ata ttg att gct tta aac
437 1099
438 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
439                280                285                290
E--> 441 cga ttt ctt cag gag aaa cat ggt tct aag atg gcc ttt ttg gat ggc
442 1147
443 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
444                295                300                305
E--> 446 aat cca ccc gaa aga ctt tgt atg cca ata gtt gat tat att cag tcc
447 1195
448 Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp Tyr Ile Gln Ser
449 310                315                320                325
E--> 451 ttg ggt ggt gaa gtt cat cta aat tcg cgc att caa aaa att gag cta
452 1243
453 Leu Gly Gly Glu Val His Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
454                330                335                340
E--> 456 aat gat gat gga acg gtg aag agc ttc tta cta aat aat ggg aaa gtg
457 1291
458 Asn Asp Asp Gly Thr Val Lys Ser Phe Leu Leu Asn Asn Gly Lys Val
459                345                350                355
E--> 463 atg gaa ggg gat gct tat gtg ttt gca act cca gtg gat att ctg aag
464 1339

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same

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Output Set: N:\CRF4\01282005\J521478.raw

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465 Met Glu Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
466          360          365          370
E--> 468 ctt ctt cta cca gat aac tgg aaa ggg att cca tat ttc cag aga ttg
469 1387
470 Leu Leu Leu Pro Asp Asn Trp Lys Gly Ile Pro Tyr Phe Gln Arg Leu
471      375          380          385
E--> 473 gat aaa tta gtt ggc gtc cca gtc ata aat gtt cac ata tgg ttt gac
474 1435
475 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
476 390          395          400          405
E--> 478 aga aaa ctg aag aac aca tat gat cac ctt ctc ttt agc aga agt ccc
479 1483
480 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro
481          410          415          420
E--> 483 ctt ctg agt gta tat gct gac atg tca gta act tgc aag gaa tat tat
484 1531
485 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
486          425          430          435
E--> 488 agc cca aac cag tca atg tta gag ttg gtt ttt gca cca gcc gaa gaa
489 1579
490 Ser Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu
491          440          445          450
E--> 493 tgg att tca cgt agt gat gat gat att att caa gcc acg atg act gag
494 1627
495 Trp Ile Ser Arg Ser Asp Asp Asp Ile Ile Gln Ala Thr Met Thr Glu
496      455          460          465
E--> 498 ctt gcc aaa ctc ttt cct gat gaa att tct gca gac caa agc aaa gca
499 1675
500 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala
501 470          475          480          485
E--> 503 aag att ctc aag tac cat gtt gtt aaa aca cca agg tcg gtt tac aaa
504 1723
505 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
506          490          495          500
E--> 508 act gtt cca aat tgt gaa cct tgt cga ccc att caa aga tct cct ata
509 1771
510 Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Ile Gln Arg Ser Pro Ile
511          505          510          515
E--> 513 gaa ggt ttc tat tta gct gga gat tac aca aaa caa aaa tat tta gct
514 1819
515 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
516      520          525          530
E--> 520 tca atg gaa ggc gct gtt ctt tct ggg aag ctt tgt gca cag gct att
521 1867
522 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile
523      535          540          545
E--> 525 gta cag gat tct gag cta cta gct act cgg ggc cag aaa aga atg gct
526 1915
527 Val Gln Asp Ser Glu Leu Leu Ala Thr Arg Gly Gln Lys Arg Met Ala

```



RAW SEQUENCE LISTING

DATE: 01/28/2005

PATENT APPLICATION: US/10/521,478

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

528 550          555          560          565
E--> 530 aaa gca agt gtt gtg taa caaaaacaag aattgaaaga gtcattggtag
531 1963
532 Lys Ala Ser Val Val
533          570
E--> 535 agtacaggag catcatttca actttggcat tctttgtctg tggtcaggac tcaggagacc
536 2023
E--> 538 ttcaacttta ttagttcata cgaataaaga aaggctcagc ttctgaaatt tagctgcacc
539 2083
E--> 541 gtcgtcaact gtgtgcaata agctatacgg aacaaacgac atgtgtcaac tttaagtcag
542 2143
E--> 544 cccattgttt tggtatcctc caattttctg gatcaatggt tgtattggaa agaaatatgt
545 2203
E--> 547 cattattcaa acttgtttat atccactttt tttatttatc aacatttgtc acaacctttc
548 2263
E--> 550 gttgagtaaa aaaaaaaaaa aaaagaattc
551 2293
639 <210> SEQ ID NO: 5
640 <211> LENGTH: 2264
641 <212> TYPE: DNA
642 <213> ORGANISM: Zea mays
644 <220> FEATURE:
645 <221> NAME/KEY: CDS
646 <222> LOCATION: (351)..(2066)
648 <400> SEQUENCE: 5
E--> 649 ctccaaatgc ggagggtctcg actcttctct ctctctccat ctttatcatc gccccacgta
650 60
E--> 652 cacacccaat tcctcgcaac tggggtcccc cgcctccacg acactgcccc ccgtctcaag
653 120
E--> 655 tccgccgcct ccattcttca gctctcctat cctccgccta gaatatcttc atcggtattt
656 180
E--> 658 taccaacctg gatcaattta ctacgatac tctgaagcgt atacatatgc catatgggaa
659 240
E--> 661 atgacttcat agctgtgggt tgtcttatgg ctcttgaat ttgcagtagt ctgcctgtac
662 300
E--> 664 ctattggctg aagcagagct gacccccact ttatcaagag ttgctcaacg atg gac
665 356
666
667 Met Asp
1
E--> 669 act ggc tgc ctg tca tct atg aat att act gga gct agc cag aca aga
670 404
671 Thr Gly Cys Leu Ser Ser Met Asn Ile Thr Gly Ala Ser Gln Thr Arg
672          5          10          15
E--> 674 tct ttt gcg ggg caa ctt cct cct cag aga tgt ttt gcg agt agt cac
675 452
676 Ser Phe Ala Gly Gln Leu Pro Pro Gln Arg Cys Phe Ala Ser Ser His
677          20          25          30
E--> 679 tat aca agc ttt gcc gtg aaa aaa ctt gtc tca agg aat aaa gga agg
680 500

```

*same**same*

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

681 Tyr Thr Ser Phe Ala Val Lys Lys Leu Val Ser Arg Asn Lys Gly Arg
682 35 40 45 50
E--> 684 aga tca cac cgt aga cat cct gcc ttg cag gtt gtc tgc aag gat ttt
685 548
686 Arg Ser His Arg Arg His Pro Ala Leu Gln Val Val Cys Lys Asp Phe
687 55 60 65
E--> 689 cca aga cct cca cta gaa agc aca ata aac tat ttg gaa gct gga cag
690 596
691 Pro Arg Pro Pro Leu Glu Ser Thr Ile Asn Tyr Leu Glu Ala Gly Gln
694 70 75 80
E--> 696 ctc tct tca ttt ttt aga aac agc gaa cgc ccc agt aag ccg ttg cag
697 644
698 Leu Ser Ser Phe Phe Arg Asn Ser Glu Arg Pro Ser Lys Pro Leu Gln
699 85 90 95
E--> 701 gtc gtg gtt gct ggt gca gga ttg gct ggt cta tca aca gcg aag tat
702 692
703 Val Val Val Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr
704 100 105 110
E--> 706 ctg gca gat gct ggc cat aaa ccc ata ttg ctt gag gca aga gat gtt
707 740
708 Leu Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val
709 115 120 125 130
E--> 711 ttg ggt gga aag gta gct gct tgg aag gat gaa gat gga gat tgg tac
712 788
713 Leu Gly Gly Lys Val Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr
714 135 140 145
E--> 716 gag act ggg ctt cat ata ttt ttt gga gct tat ccc aac ata cag aat
717 836
718 Glu Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn
719 150 155 160
E--> 721 ctg ttt ggc gag ctt agg att gag gat cgt ttg cag tgg aaa gaa cac
722 884
723 Leu Phe Gly Glu Leu Arg Ile Glu Asp Arg Leu Gln Trp Lys Glu His
724 165 170 175
E--> 726 tct atg ata ttc gcc atg cca aac aag cca gga gaa ttc agc cgg ttc
727 932
728 Ser Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe
729 180 185 190
E--> 731 gat ttc cca gaa act ttg cca gca cct ata aat ggg ata tgg gcc ata
732 980
733 Asp Phe Pro Glu Thr Leu Pro Ala Pro Ile Asn Gly Ile Trp Ala Ile
734 195 200 205 210
E--> 736 ttg aga aac aat gaa atg ctt act tgg ccg gag aag gtg aag ttt gca
737 1028
738 Leu Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala
739 215 220 225
E--> 741 atc gga ctt ctg cca gca atg gtt ggt ggt caa cct tat gtt gaa gct
742 1076
743 Ile Gly Leu Leu Pro Ala Met Val Gly Gly Gln Pro Tyr Val Glu Ala

```

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

      744          230          235          240
E--> 746  caa gat ggc tta acc gtt tca gaa tgg atg aaa aag cag ggt gtt cct
      747 1124
      748 Gln Asp Gly Leu Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro
      749          245          250          255
E--> 753  gat cgg gtg aac gat gag gtt ttt att gca atg tcc aag gca ctc aat
      754 1172
      755 Asp Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn
      756          260          265          270
E--> 758  ttc ata aat cct gat gag cta tct atg cag tgc att ttg att gct ttg
      759 1220
      760 Phe Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu
      761 275          280          285          290
E--> 763  aac cga ttt ctt cag gag aag cat ggt tct aaa atg gca ttc ttg gat
      764 1268
      765 Asn Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp
      766          295          300          305
E--> 768  ggt aat ccg cct gaa agg cta tgc atg cct att gtt gat cac att cgg
      769 1316
      770 Gly Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Ile Arg
      771          310          315          320
E--> 773  tct agg ggt gga gag gtc cgc ctg aat tct cgt att aaa aag ata gag
      774 1364
      775 Ser Arg Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Lys Lys Ile Glu
      776          325          330          335
E--> 778  ctg aat cct gat gga act gta aaa cac ttc gca ctt agt gat gga act
      779 1412
      780 Leu Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Ser Asp Gly Thr
      781          340          345          350
E--> 783  caa ata act gga gat gct tat gtt tgt gca aca cca gtc gat atc ttc
      784 1460
      785 Gln Ile Thr Gly Asp Ala Tyr Val Cys Ala Thr Pro Val Asp Ile Phe
      786 355          360          365          370
E--> 788  aag ctt ctt gta cct caa gag tgg agt gaa att act tat ttc aag aaa
      789 1508
      790 Lys Leu Leu Val Pro Gln Glu Trp Ser Glu Ile Thr Tyr Phe Lys Lys
      791          375          380          385
E--> 793  ctg gag aag ttg gtg gga gtt cct gtt atc aat gtt cat ata tgg ttt
      794 1556
      795 Leu Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe
      796          390          395          400
E--> 798  gac aga aaa ctg aac aac aca tat gac cac ctt ctt ttc agc agg agt
      799 1604
      800 Asp Arg Lys Leu Asn Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser
      801          405          410          415
E--> 803  tca ctt tta agt gtc tat gca gac atg tca gta acc tgc aag gaa tac
      804 1652
      805 Ser Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr
      806          420          425          430

```

same

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TIME: 11:37:36

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

E--> 810 tat gac cca aac cgt tca atg ctg gag ttg gtc ttt gct cct gca gac
      811 1700
      812 Tyr Asp Pro Asn Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Asp
      813 435                440                445                450
E--> 815 gaa tgg att ggt cga agt gac act gaa atc atc gat gca act atg gaa
      816 1748
      817 Glu Trp Ile Gly Arg Ser Asp Thr Glu Ile Ile Asp Ala Thr Met Glu
      818                455                460                465
E--> 820 gag cta gcc aag tta ttt cct gat gaa att gct gct gat cag agt aaa
      821 1796
      822 Glu Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys
      823                470                475                480
E--> 825 gca aag att ctt aag tat cat att gtg aag aca ccg aga tcg gtt tac
      826 1844
      827 Ala Lys Ile Leu Lys Tyr His Ile Val Lys Thr Pro Arg Ser Val Tyr
      828                485                490                495
E--> 830 aaa act gtc cca aac tgt gag cct tgc cgg cct ctc caa agg tca cct
      831 1892
      832 Lys Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro
      833                500                505                510
E--> 835 atc gaa ggt ttc tat cta gct ggt gat tac aca aag cag aaa tac ctg
      836 1940
      837 Ile Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu
      838 515                520                525                530
E--> 840 gct tct atg gaa ggt gca gtc cta tcc ggg aag ctt tgt gcc cag tcc
      841 1988
      842 Ala Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser
      843                535                540                545
E--> 845 ata gtg cag gat tat agc agg ctc gca ctc agg agc cag aaa agc cta
      846 2036
      847 Ile Val Gln Asp Tyr Ser Arg Leu Ala Leu Arg Ser Gln Lys Ser Leu
      848                550                555                560
E--> 850 caa tca gga gaa gtt ccc gtc cca tct tag ttgtagttgg ctttagctat
      851 2086
      852 Gln Ser Gly Glu Val Pro Val Pro Ser
      853                565                570
E--> 855 cgtcatcccc actgggtgct atcttatctc ctatttcaat gggaaccac ccaatggtca
      856 2146
E--> 858 tgttgagac aacacctgtt atggtccttt gaccatctcg tgggtgactgt agttgatgct
      859 2206
E--> 861 atattcggat atatatgtaa aaggacctgc atagcaattg ttagaccttg gaaaaaaaa
      862 2264
950 <210> SEQ ID NO: 7
951 <211> LENGTH: 2027
952 <212> TYPE: DNA
953 <213> ORGANISM: Oryza sativa
955 <220> FEATURE:
956 <221> NAME/KEY: CDS
957 <222> LOCATION: (5)..(1705)

```

RAW SEQUENCE LISTING

DATE: 01/28/2005

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TIME: 11:37:36

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

959 <400> SEQUENCE: 7

```

E--> 960 gttt atg aca gca tct gcc aga tat ttt gca gga caa ctt cct act cat
961 49
962      Met Thr Ala Ser Ala Arg Tyr Phe Ala Gly Gln Leu Pro Thr His
963      1          5          10          15
E--> 965 agg tgc ttc gca agt agc agc atc caa gca ctg aaa ggt agt cag cat
966 97
967 Arg Cys Phe Ala Ser Ser Ser Ile Gln Ala Leu Lys Gly Ser Gln His
968      20          25          30
E--> 970 gtg agc ttt gga gtg aaa tct ctt gtc tta agg aat aaa gga aaa aga
971 145
972 Val Ser Phe Gly Val Lys Ser Leu Val Leu Arg Asn Lys Gly Lys Arg
973      35          40          45
E--> 975 ttc cgt cgg agg ctc ggt gct cta cag gtt gtt tgc cag gac ttt cca
976 193
977 Phe Arg Arg Arg Leu Gly Ala Leu Gln Val Val Cys Gln Asp Phe Pro
978      50          55          60
E--> 980 aga cct cca cta gaa aac aca ata aac ttt ttg gaa gct gga caa cta
981 241
984 Arg Pro Pro Leu Glu Asn Thr Ile Asn Phe Leu Glu Ala Gly Gln Leu
985      65          70          75
E--> 987 tcc tca ttt ttc aga aac agt gaa caa ccc act aaa cca tta cag gtc
988 289
989 Ser Ser Phe Phe Arg Asn Ser Glu Gln Pro Thr Lys Pro Leu Gln Val
990 80          85          90          95
E--> 992 gtg att gct gga gca gga tta gct ggt tta tca acg gca aaa tat ctg
993 337
994 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
995      100          105          110
E--> 997 gca gat gct ggt cat aaa ccc ata ttg ctt gag gca agg gat gtt ttg
998 385
999 Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
1000      115          120          125
E--> 1002 ggt gga aag ata gct gct tgg aag gat gaa gat gga gat tgg tat gaa
1003 433
1004 Gly Gly Lys Ile Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr Glu
1005      130          135          140
E--> 1007 act ggg ctt cat atc ttt ttt gga gct tat ccc aac ata cag aac ttg
1008 481
1009 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn Leu
1010      145          150          155
E--> 1012 ttt ggc gag ctt ggt att aat gat cgg ttg caa tgg aag gaa cac tcc
1013 529
1014 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
1015 160          165          170          175
E--> 1017 atg ata ttt gcc atg cca aac aag cca gga gaa tcc agc cgg ttt gat
1018 577
1019 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Ser Ser Arg Phe Asp
1020      180          185          190

```

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

E--> 1022 ttt cct gaa aca ttg cct gca ccc tta aat gga ata tgg gcc ata cta
      1023 625
      1024 Phe Pro Glu Thr Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu
      1025          195          200          205
E--> 1027 aga aac aat gaa atg cta act tgg cca gag aag gtg aag ttt gct ctt
      1028 673
      1029 Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Leu
      1030          210          215          220
E--> 1032 gga ctt ttg cca gca atg gtt ggt ggc caa gct tat gtt gaa gct caa
      1033 721
      1034 Gly Leu Leu Pro Ala Met Val Gly Gly Gln Ala Tyr Val Glu Ala Gln
      1035          225          230          235
E--> 1037 gat ggt ttt act gtt tct gag tgg atg aaa aag cag ggt gtt cct gat
      1038 769
      1039 Asp Gly Phe Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro Asp
      1042 240          245          250          255
E--> 1044 cga gtg aac gat gaa gtt ttc att gca atg tca aag gca ctt aat ttc
      1045 817
      1046 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
      1047          260          265          270
E--> 1049 ata aat cct gat gag tta tcc atg cag tgc att ctg att gct tta aac
      1050 865
      1051 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
      1052          275          280          285
E--> 1054 cga ttt ctt cag gag aag cat ggt tct aag atg gca ttc ttg gat ggt
      1055 913
      1056 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
      1057          290          295          300
E--> 1059 aat cct cct gaa agg tta tgc atg cct att gtt gac cat gtt cgc tct
      1060 961
      1061 Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Val Arg Ser
      1062          305          310          315
E--> 1064 ttg ggt ggt gag gtt cgg ctg aat tct cgt att cag aaa ata gaa ctt
      1065 1009
      1066 Leu Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
      1067 320          325          330          335
E--> 1069 aat cct gat gga aca gtg aaa cac ttt gca ctt acc gat gga act caa
      1070 1057
      1071 Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Thr Asp Gly Thr Gln
      1072          340          345          350
E--> 1074 ata act gga gat gct tat gtt ttt gca aca cca gtt gat atc ttg aag
      1075 1105
      1076 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
      1077          355          360          365
E--> 1079 ctt ctt gta cct caa gag tgg aaa gaa ata tct tat ttc aag aag ctg
      1080 1153
      1081 Leu Leu Val Pro Gln Glu Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu
      1082          370          375          380
E--> 1084 gag aag ttg gtg gga gtt cct gtt ata aat gtt cat ata tgg ttt gat

```



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/521,478

DATE: 01/28/2005

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

```

1085 1201
1086 Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
1087      385                      390                      395
E--> 1089 aga aaa ctg aag aac aca tat gac cac ctt ctt ttc agc agg agt tca
1090 1249
1091 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Ser
1092 400                      405                      410                      415
E--> 1094 ctt tta agt gtt tat gcg gac atg tca gta act tgc aag gaa tac tat
1095 1297
1096 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
1097                      420                      425                      430
E--> 1101 gat cca agc cgt tca atg ctg gag ttg gtc ttt gct cct gca gag gaa
1102 1345
1103 Asp Pro Ser Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu
1104                      435                      440                      445
E--> 1106 tgg gtt gga cgg agt gac act gaa atc atc gaa gca act atg caa gag
1107 1393
1108 Trp Val Gly Arg Ser Asp Thr Glu Ile Ile Glu Ala Thr Met Gln Glu
1109                      450                      455                      460
E--> 1111 cta gcc aag cta ttt cct gat gaa att gct gct gat cag agt aaa gca
1112 1441
1113 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys Ala
1114                      465                      470                      475
E--> 1116 aag att ctg aag tat cat gtt gtg aag aca cca aga tct gtt tac aag
1117 1489
1118 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
1119 480                      485                      490                      495
E--> 1121 act atc ccg gac tgt gaa cct tgc cga cct ctg caa aga tca ccg att
1122 1537
1123 Thr Ile Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile
1124                      500                      505                      510
E--> 1126 gaa ggg ttc tat cta gct ggt gac tac aca aag cag aaa tat ttg gct
1127 1585
1128 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
1129                      515                      520                      525
E--> 1131 tcg atg gag ggt gca gtt cta tct ggg aag ctt tgt gct cag tct gta
1132 1633
1133 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser Val
1134                      530                      535                      540
E--> 1136 gtg gag gat tat aaa atg cta tct cgt agg agc ctg aaa agt ctg cag
1137 1681
1138 Val Glu Asp Tyr Lys Met Leu Ser Arg Arg Ser Leu Lys Ser Leu Gln
1139                      545                      550                      555
E--> 1141 tcc gaa gtt cct gtt gcc tcc tag ttgtagtcag gactattccc aatgggtgtgt
1142 1735
1143 Ser Glu Val Pro Val Ala Ser
1144 560                      565
E--> 1146 gtgtcatcat cccctagtca gtttttttct atttagtggg tgcccaactc tccaccaatt
1147 1795

```



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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

E--> 1149 tacacatgat ggaacttgaa agatgcctat tttggtctta tcatatttct gtaaagttga
1150 1855
E--> 1152 tttgtgactg agagctgatg ccgatatgcc acgctggaga aaaagaacat tatgtaaaac
1153 1915
E--> 1157 gacctgcata gtaattctta gacttttgca aaaggcaaaa ggggtaaagc gacctttttt
1158 1975
E--> 1160 ttctatgtga agggattaag agaccttaaa aaaaaaaaaa aaaaaaaaaa aa
1161 2027



VERIFICATION SUMMARY

DATE: 01/28/2005

PATENT APPLICATION: US/10/521,478

TIME: 11:37:37

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\01282005\J521478.raw

L:13 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:333 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:649 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
M:254 Repeated in SeqNo=5
L:960 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:49 SEQ:7
M:254 Repeated in SeqNo=7